Complete Genome Sequence of the Marine Cellulose- and Xylan-Degrading Bacterium *Glaciecola* sp. Strain 4H-3-7+YE-5

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*Glaciecola* sp. strain 4H-3-7+YE-5 was isolated from subseafloor sediments at Suruga Bay in Japan and is capable of efficiently hydrolyzing cellulose and xylan. The complete genome sequence of *Glaciecola* sp. 4H-3-7+YE-5 revealed several genes encoding putatively novel glycoside hydrolases, offering a high potential for plant biomass degradation.

Members of the genus *Glaciecola* are Gram-negative, aerobic, and halotolerant bacteria (3) that can be found in various marine habitats (1, 4, 11–15, 17, 18). *Glaciecola* sp. 4H-3-7+YE-5 was isolated from marine subseafloor sediments (31.4 m below the seafloor) collected at a water depth of 755 m at Suruga Bay (Japan) after enrichment on cellulose, xylan, and chitin as sole carbon sources. Until now, little was known about the cellulolytic and hemicellulolytic enzyme systems of *Glaciecola* spp., since only one endo-beta-1,4-xylanase from the cellulolytic and hemicellulolytic enzyme systems of *G.* *mesophilica* has been described (2). In order to gain insight into the complete gene repertoire of *Glaciecola* sp. 4H-3-7+YE-5, the genome was sequenced at the DOE Joint genome Institute (JGI) using a combination of Illumina (2) and 454 technologies (10). To this end, we constructed and sequenced an Illumina GAii shotgun library which generated 50,060,436 reads totaling 3,804 Mb, as well as a 454 Titanium standard library which generated 233,681 reads which generated 50,060,436 reads totaling 3,804 Mb, as well as a 454 Titanium standard library which generated 233,681 reads totaling 164.4 Mb. All general aspects of Illumina construction and sequencing can be found at http://www.jgi.doe.gov/. The initial draft assembly contained 55 contigs in 2 scaffolds. The 454 Titanium standard data and the 454 paired-end 454 libraries with average insert sizes of 10.0 kb, 5.4 kb, and 5.9 kb which generated 272,557 reads totaling 137.8 Mb of 454 draft data which provides 25.6x average genome coverage and 1,774 Mb of Illumina draft data which provides 329x average genome coverage.

The genome of *Glaciecola* sp. 4H-3-7+YE-5 is contained within one large chromosome (5,052,309 bp) and one plasmid (pGLAAG01, 341,282 bp). The complete genome has a total G+C content of 45% and comprises 4,548 predicted protein-encoding ORFs.

This is the first complete genome sequence for a member of the genus *Glaciecola*. In-depth analysis revealed the presence of numerous ORFs encoding carbohydrate-active enzymes, including glycoside hydrolases, glycolytransferases, and carbohydrate esterases, making the organism a promising source of biocatalysts needed for polysaccharide degradation.

**Nucleotide sequence accession numbers.** The complete chromosome and plasmid sequences of *Glaciecola* sp. 4H-3-7+YE-5 have been deposited in GenBank under accession numbers CP002526 and CP002527.

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REFERENCES


